

RAW SEQUENCE LISTING

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Application Serial Number: 10/664, 801 A
Source: JFW16
Date Processed by STIC: 09/25/2006

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IFW16

RAW SEQUENCE LISTING

DATE: 09/25/2006

PATENT APPLICATION: US/10/664,801A

TIME: 09:05:46

Input Set : A:\2006-09-18 4614-0120P seq list.txt

Output Set: N:\CRF4\09252006\J664801A.raw

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4 <110> APPLICANT: HALKIER, Torben
5   HAANING, Jesper
7 <120> TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand Activity
9 <130> FILE REFERENCE: 3631-0114P
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/664,801A
C--> 12 <141> CURRENT FILING DATE: 2003-09-17
14 <160> NUMBER OF SEQ ID NOS: 36
16 <170> SOFTWARE: PatentIn Ver. 2.1
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 2271
20 <212> TYPE: DNA
21 <213> ORGANISM: Homo sapiens
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (185)..(1138)
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29 aaagccgggc tccaagtcgg cgccccacgt cgaggtccg ccgcagcctc cggagttggc 120
30 cgcagacaag aaggggaggg agcgggagag ggaggagagc tccgaagcga gagggccgag 180
31 cgcc atg cgc cgc gcc agc aga gac tac acc aag tac ctg cgt ggc tcg 229
32   Met Arg Arg Ala Ser Arg Asp Tyr Thr Lys Tyr Leu Arg Gly Ser
33       1           5           10           15
34 gag gag atg ggc ggc ggc ccc gga gcc ccg cac gag ggc ccc ctg cac 277
35 Glu Glu Met Gly Gly Gly Pro Gly Ala Pro His Glu Gly Pro Leu His
36           20           25           30
37 gcc ccg ccg ccg cct gcg ccg cac cag ccc ccc gcc gcc tcc cgc tcc 325
38 Ala Pro Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser
39           35           40           45
40 atg ttc gtg gcc ctc ctg ggg ctg ggg ctg ggc cag gtt gtc tgc agc 373
41 Met Phe Val Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser
42           50           55           60
43 gtc gcc ctg ttc ttc tat ttc aga gcg cag atg gat cct aat aga ata 421
44 Val Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile
45           65           70           75
46 tca gaa gat ggc act cac tgc att tat aga att ttg aga ctc cat gaa 469
47 Ser Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu
48 80           85           90           95
49 aat gca gat ttt caa gac aca act ctg gag agt caa gat aca aaa tta 517
50 Asn Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu
51           100           105           110
52 ata cct gat tca tgt agg aga att aaa cag gcc ttt caa gga gct gtg 565
53 Ile Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val
54           115           120           125

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55 caa aag gaa tta caa cat atc gtt gga tca cag cac atc aga gca gag 613
56 Gln Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu
57      130      135      140
58 aaa gcg atg gtg gat ggc tca tgg tta gat ctg gcc aag agg agc aag 661
59 Lys Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys
60      145      150      155
61 ctt gaa gct cag cct ttt gct cat ctc act att aat gcc acc gac atc 709
62 Leu Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile
63 160      165      170      175
64 cca tct ggt tcc cat aaa gtg agt ctg tcc tct tgg tac cat gat cgg 757
65 Pro Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg
66      180      185      190
67 ggt tgg gcc aag atc tcc aac atg act ttt agc aat gga aaa cta ata 805
68 Gly Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile
69      195      200      205
70 gtt aat cag gat ggc ttt tat tac ctg tat gcc aac att tgc ttt cga 853
71 Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg
72      210      215      220
73 cat cat gaa act tca gga gac cta gct aca gag tat ctt caa cta atg 901
74 His His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met
75      225      230      235
76 gtg tac gtc act aaa acc agc atc aaa atc cca agt tct cat acc ctg 949
77 Val Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu
78 240      245      250      255
79 atg aaa gga gga agc acc aag tat tgg tca ggg aat tct gaa ttc cat 997
80 Met Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His
81      260      265      270
82 ttt tat tcc ata aac gtt ggt gga ttt ttt aag tta cgg tct gga gag 1045
83 Phe Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu
84      275      280      285
85 gaa atc agc atc gag gtc tcc aac ccc tcc tta ctg gat ccg gat cag 1093
86 Glu Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln
87      290      295      300
88 gat gca aca tac ttt ggg gct ttt aaa gtt cga gat ata gat tga 1138
89 Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp
90      305      310      315
91 gccccagttt ttggagtgtt atgtatttcc tggatgtttg gaaacatttt ttaaaacaag 1198
92 ccaagaaaga tgtatatagg tgtgtgagac tactaagagg catggcccca acggtacacg 1258
93 actcagtatc catgctcttg acctgttaga gaacacgcgt atttacagcc agtgggagat 1318
94 gttagactca tgggtgtgta cacaatggtt tttaaatttt gtaatgaatt cctagaatta 1378
95 aaccagattg gagcaattac gggttgacct tatgagaaac tgcattgtggg ctatgggagg 1438
96 ggttggtccc tgggtcatgtg ccccttcgca gctgaagtgg agaggggtgtc atctagcgca 1498
97 attgaaggat catctgaagg ggcaaattct tttgaattgt tacatcatgc tggaaacctgc 1558
98 aaaaaatact ttttctaata aggagagaaa atatatgtat ttttatataa tatctaaagt 1618
99 tatatttcag atgtaatgtt ttctttgcaa agtattgtaa attatatttg tgctatagta 1678
100 tttgattcaa aatattttaa aatgtcttgc tgttgacata tttaatgttt taaatgtaca 1738
101 gacatattta actggtgcac tttgtaaatt ccctggggaa aacttgcagc taaggagggg 1798
102 aaaaaaatgt tgtttcctaa tatcaaagtc agtatatttc ttcgttcttt ttaagttaat 1858
103 agattttttc agacttgtca agcctgtgca aaaaaattaa aatggatgcc ttgaataata 1918

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104 agcaggatgt tggccaccag gtgcctttca aatttagaaa ctaattgact ttagaaagct 1978
105 gacattgccca aaaaggatac ataatgggcc actgaaatct gtcaagagta gttatataat 2038
106 tgttgaacag gtgtttttcc acaagtgccg caaattgtac cttttttttt ttttcaaaat 2098
107 agaaaagtta ttagtggttt atcagcaaaa aagtccaatt ttaatttagt aaatgttatc 2158
108 ttatactgta caataaaaaac attgcctttg aatgttaatt ttttggtaca aaaataaatt 2218
109 tatatgaaaa aaaaaaaaaa agggcgggccg ctctagaggg ccctattcta tag 2271
112 <210> SEQ ID NO: 2
113 <211> LENGTH: 317
114 <212> TYPE: PRT
115 <213> ORGANISM: Homo sapiens :
117 <400> SEQUENCE: 2
118 Met Arg Arg Ala Ser Arg Asp Tyr Thr Lys Tyr Leu Arg Gly Ser Glu
119 1 5 10 15
120 Glu Met Gly Gly Gly Pro Gly Ala Pro His Glu Gly Pro Leu His Ala
121 20 25 30
122 Pro Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser Met
123 35 40 45
124 Phe Val Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser Val
125 50 55 60
126 Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser
127 65 70 75 80
128 Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu Asn
129 85 90 95
130 Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu Ile
131 100 105 110
132 Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val Gln
133 115 120 125
134 Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu Lys
135 130 135 140
136 Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu
137 145 150 155 160
138 Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile Pro
139 165 170 175
140 Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg Gly
141 180 185 190
142 Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile Val
143 195 200 205
144 Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
145 210 215 220
146 His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met Val
147 225 230 235 240
148 Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu Met
149 245 250 255
150 Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His Phe
151 260 265 270
152 Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu Glu
153 275 280 285
154 Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp
155 290 295 300

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157 305          310          315
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162 <211> LENGTH: 951
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164 <213> ORGANISM: Mus musculus
166 <220> FEATURE:
167 <221> NAME/KEY: CDS
168 <222> LOCATION: (1)..(951)
170 <220> FEATURE:
171 <221> NAME/KEY: misc_feature
172 <222> LOCATION: (142)..(213)
173 <223> OTHER INFORMATION: Transmembrane domain
175 <220> FEATURE:
176 <221> NAME/KEY: misc_feature
177 <222> LOCATION: (454)..(948)
178 <223> OTHER INFORMATION: Tumour Necrosis Factor(TNF)-like domain
180 <400> SEQUENCE: 3
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182 Met Arg Arg Ala Ser Arg Asp Tyr Gly Lys Tyr Leu Arg Ser Ser Glu
183 1 5 10 15
184 gag atg ggc agc ggc ccc ggc gtc cca cac gag ggt ccg ctg cac ccc 96
185 Glu Met Gly Ser Gly Pro Gly Val Pro His Glu Gly Pro Leu His Pro
186 20 25 30
187 gcg cct tct gca ccg gct ccg gcg ccg cca ccc gcc gcc tcc cgc tcc 144
188 Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser
189 35 40 45
190 atg ttc ctg gcc ctc ctg ggg ctg gga ctg ggc cag gtg gtc tgc agc 192
191 Met Phe Leu Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser
192 50 55 60
193 atc gct ctg ttc ctg tac ttt cga gcg cag atg gat cct aac aga ata 240
194 Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile
195 65 70 75 80
196 tca gaa gac agc act cac tgc ttt tat aga atc ctg aga ctc cat gaa 288
197 Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu
198 85 90 95
199 aac gca ggt ttg cag gac tcg act ctg gag agt gaa gac aca cta cct 336
200 Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro
201 100 105 110
202 gac tcc tgc agg agg atg aaa caa gcc ttt cag ggg gcc gtg cag aag 384
203 Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys
204 115 120 125
205 gaa ctg caa cac att gtg ggg cca cag cgc ttc tca gga gct cca gct 432
206 Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala
207 130 135 140
208 atg atg gaa ggc tca tgg ttg gat gtg gcc cag cga ggc aag cct gag 480
209 Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu
210 145 150 155 160
211 gcc cag cca ttt gca cac ctc acc atc aat gct gcc agc atc cca tcg 528

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Input Set : A:\2006-09-18 4614-0120P seq list.txt

Output Set: N:\CRF4\09252006\J664801A.raw

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212 Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser
213          165          170          175
214 ggt tcc cat aaa gtc act ctg tcc tct tgg tac cac gat cga ggc tgg 576
215 Gly Ser His Lys Val Thr Leu Ser Ser Trp Tyr His Asp Arg Gly Trp
216          180          185          190
217 gcc aag atc tct aac atg acg tta agc aac gga aaa cta agg gtt aac 624
218 Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn
219          195          200          205
220 caa gat ggc ttc tat tac ctg tac gcc aac att tgc ttt cgg cat cat 672
221 Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His
222          210          215          220
223 gaa aca tcg gga agc gta cct aca gac tat ctt cag ctg atg gtg tat 720
224 Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr
225 225          230          235          240
226 gtc gtt aaa acc agc atc aaa atc cca agt tct cat aac ctg atg aaa 768
227 Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys
228          245          250          255
229 gga ggg agc acg aaa aac tgg tcg ggc aat tct gaa ttc cac ttt tat 816
230 Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr
231          260          265          270
232 tcc ata aat gtt ggg gga ttt ttc aag ctc cga gct ggt gaa gaa att 864
233 Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile
234          275          280          285
235 agc att cag gtg tcc aac cct tcc ctg ctg gat ccg gat caa gat gcg 912
236 Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala
237          290          295          300
238 acg tac ttt ggg gct ttc aaa gtt cag gac ata gac tga 951
239 Thr Tyr Phe Gly Ala Phe Lys Val Gln Asp Ile Asp
240 305          310          315
243 <210> SEQ ID NO: 4
244 <211> LENGTH: 316
245 <212> TYPE: PRT
246 <213> ORGANISM: Mus musculus
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252 20 25 30
253 Ala Pro Ser Ala Pro Ala Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser
254 35 40 45
255 Met Phe Leu Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser
256 50 55 60
257 Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile
258 65 70 75 80
259 Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu
260 85 90 95
261 Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro
262 100 105 110
263 Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys

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VERIFICATION SUMMARY

DATE: 09/25/2006

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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date